

02DO

#2

OIPE

RAW SEQUENCE LISTING DATE: 07/05/2000
 PATENT APPLICATION: US/09/599,760 TIME: 18:57:37

Input Set : A:\464428_1.txt
 Output Set: N:\CRF3\07052000\I599760.raw

ENTERED

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4 <110> APPLICANT: Newell, Martha K.
6 <120> TITLE OF INVENTION: Methods and Products for Manipulating
7   Uncoupling Protein Expression in the Plasma Membrane
10 <130> FILE REFERENCE: I0277/7009
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/599,760
C--> 12 <141> CURRENT FILING DATE: 2000-06-22
12 <150> PRIOR APPLICATION NUMBER: US 60/140,574
13 <151> PRIOR FILING DATE: 1999-06-23
15 <160> NUMBER OF SEQ ID NOS: 6
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20 <211> LENGTH: 924
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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26 ggaatagcgg cgtgcttgcc ggacgtgac accttccccgc tggacacggc caaagtcagg    120
27 ctccagggtcc aaggtgaatg cccgacgtcc agtggtatta ggtataaagg tgcctggga    180
28 acaatcacgg ctgtggtaaa aacagaaggc cggatgaaac tctacagcgg gctgcctgcg    240
29 gggcttcagc ggcaaatcag ctccgcctct ctcaggatcg gcctctacga cacgggtccag    300
30 gagttcctca ccgcagggaa agaaacagca cctagttagt gaagcaagat tttagctggt    360
31 ctaacgactg gagagtggtc agtattcatt gggcaaccca cagaggtcgt gaaagtcaga    420
32 cttaagcac agagccatct ccacggaatc aaacctcgct acacggggac ttataatgcg    480
33 tacagaataa tagcaacaac cgaaggcttg acgggtcttt ggaaagggac tactccaat    540
34 ctgatgagaa gtgtcatcat caattgtaca gagctagtaa catatgatct aatgaaggag    600
35 gcctttgtga aaaacaacat attagcagat gacgtccccct gccacttggt gtcggctctt    660
36 atcgctggat ttgctgcaac agctatgtcc tccccggtgg atgtagtaaa aaccagattt    720
37 attaatcttc caccaggaca gtacaaaagt gtgcccact gtgcaatgaa agtggttact    780
38 aacgaaggac caacggcttt ctcaagggg ttggtacct ccttcttgcg acttgatcc    840
39 tggaaacgtc ttatgtttgt gtgctttgaa caactgaaac gagaactgtc aaagtcaagg    900
40 cagactatgg actgtgccac ataa
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43 <211> LENGTH: 307
44 <212> TYPE: PRT
45 <213> ORGANISM: Homo sapiens
47 <400> SEQUENCE: 2
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50 Leu Phe Ser Ala Gly Ile Ala Ala Cys Leu Ala Asp Val Ile Thr Phe
51   20          25          30
52 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Val Gln Gly Glu Cys Pro
53   35          40          45
54 Thr Ser Ser Val Ile Arg Tyr Lys Gly Val Leu Gly Thr Ile Thr Ala
55   50          55          60
56 Val Val Lys Thr Glu Gly Arg Met Lys Leu Tyr Ser Gly Leu Pro Ala
57   65          70          75          80
58 Gly Leu Gln Arg Gln Ile Ser Ser Ala Ser Leu Arg Ile Gly Leu Tyr

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59				85				90				95				
60	Asp	Thr	Val	Gln	Glu	Phe	Leu	Thr	Ala	Gly	Lys	Glu	Thr	Ala	Pro	Ser
61				100				105				110				
62	Leu	Gly	Ser	Lys	Ile	Leu	Ala	Gly	Leu	Thr	Thr	Gly	Gly	Val	Ala	Val
63				115				120				125				
64	Phe	Ile	Gly	Gln	Pro	Thr	Glu	Val	Val	Lys	Val	Arg	Leu	Gln	Ala	Gln
65				130				135				140				
66	Ser	His	Leu	His	Gly	Ile	Lys	Pro	Arg	Tyr	Thr	Gly	Thr	Tyr	Asn	Ala
67				145			150					155				160
68	Tyr	Arg	Ile	Ile	Ala	Thr	Thr	Glu	Gly	Leu	Thr	Gly	Leu	Trp	Lys	Gly
69				165				170				175				
70	Thr	Thr	Pro	Asn	Leu	Met	Arg	Ser	Val	Ile	Ile	Asn	Cys	Thr	Glu	Leu
71				180				185				190				
72	Val	Thr	Tyr	Asp	Leu	Met	Lys	Glu	Ala	Phe	Val	Lys	Asn	Asn	Ile	Leu
73				195				200				205				
74	Ala	Asp	Asp	Val	Pro	Cys	His	Leu	Val	Ser	Ala	Leu	Ile	Ala	Gly	Phe
75				210			215					220				
76	Cys	Ala	Thr	Ala	Met	Ser	Ser	Pro	Val	Asp	Val	Val	Lys	Thr	Arg	Phe
77				225			230					235				240
78	Ile	Asn	Ser	Pro	Pro	Gly	Gln	Tyr	Lys	Ser	Val	Pro	Asn	Cys	Ala	Met
79				245				250				255				
80	Lys	Val	Phe	Thr	Asn	Glu	Gly	Pro	Thr	Ala	Phe	Phe	Lys	Gly	Leu	Val
81				260				265				270				
82	Pro	Ser	Phe	Leu	Arg	Leu	Gly	Ser	Trp	Asn	Val	Ile	Met	Phe	Val	Cys
83				275			280					285				
84	Phe	Glu	Gln	Leu	Lys	Arg	Glu	Leu	Ser	Lys	Ser	Arg	Gln	Thr	Met	Asp
85				290			295					300				
86	Cys	Ala	Thr													
87	305															
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90	<211>	LENGTH:	1105													
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97	tactgccact	gtgaagtttc	ttggggctgg	cacagctgcc	tgcatcgag	atctcatcac										180
98	ctttcctctg	gatactgcta	aagtccggtt	acagatccaa	ggagaaagtc	aggggccagt										240
99	gcgcgctaca	gccagcgccc	agtaccgcgg	tgtgatgggc	accattctga	ccatggtgcg										300
100	tactgagggc	ccccgaagcc	tctacaatgg	gctggttgcc	ggcctgcagc	gccaaatgag										360
101	ctttgccctc	gtccgcatcg	gcctgtatga	ttctgtcaaa	cagttctaca	ccaagggctc										420
102	tgagcatgcc	agcattggga	gccgcctcct	agcaggcagc	accacagggtg	ccctggctgt										480
103	ggctgtggcc	cagcccaagg	atgtggtaaa	ggtccgattc	caagctcagg	cccgggctgg										540
104	aggtggctcg	agataccaaa	gcaccgtcaa	tgctacaag	accattgccc	gagaggaagg										600
105	gttcggggc	ctctggaaag	ggacctctcc	caatgttgct	cgtaatgcca	ttgtcaactg										660
106	tgctgagctg	gtgacctatg	acctcatcaa	ggatgccctc	ctgaaagcca	acctcatgac										720
107	agatgacctc	ccttgccact	tcacttctgc	ctttggggca	ggcttctgca	ccactgtcat										780
108	cgctccctc	gtagacgtgg	tcaagacgag	atacatgaac	tctgccctgg	gccagtacag										840
109	tagcgctggc	cactgtgccc	ttaccatgct	ccagaaggag	gggccccgag	ccttctacaa										900

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110 aggggttcacg cccctccttc tccgcttggg ttcttggaac gtggtgatgt tcgtcaccta 960
111 tgagcagctg aaacgagccc tcattgctgc ctgcacttcc cgagaggctc ccttctgagc 1020
112 ctctcctgct gctgacctga tcacctctgg ctttgtctct agccgggcca tgctttcctt 1080
113 ttcttccttc tttctcttcc ctcg 1105
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116 <211> LENGTH: 309
117 <212> TYPE: PRT
118 <213> ORGANISM: Homo sapiens
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123 Phe Leu Gly Ala Gly Thr Ala Ala Cys Ile Ala Asp Leu Ile Thr Phe
124 20 25 30
125 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Ser Gln
126 35 40 45
127 Gly Pro Val Arg Ala Thr Ala Ser Ala Gln Tyr Arg Gly Val Met Gly
128 50 55 60
129 Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro Arg Ser Leu Tyr Asn
130 65 70 75 80
131 Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Val Arg
132 85 90 95
133 Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr Thr Lys Gly Ser Glu
134 100 105 110
135 His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly Ser Thr Thr Gly Ala
136 115 120 125
137 Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
138 130 135 140
139 Gln Ala Gln Ala Arg Ala Gly Gly Arg Arg Tyr Gln Ser Thr Val
140 145 150 155 160
141 Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Gly Phe Arg Gly Leu Trp
142 165 170 175
143 Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala Ile Val Asn Cys Ala
144 180 185 190
145 Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala Leu Leu Lys Ala Asn
146 195 200 205
147 Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr Ser Ala Phe Gly Ala
148 210 215 220
149 Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val Asp Val Val Lys Thr
150 225 230 235 240
151 Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser Ser Ala Gly His Cys
152 245 250 255
153 Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg Ala Phe Tyr Lys Gly
154 260 265 270
155 Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Val Met Phe
156 275 280 285
157 Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met Ala Ala Cys Thr Ser
158 290 295 300
159 Arg Glu Ala Pro Phe
160 305

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163 <211> LENGTH: 1132
164 <212> TYPE: DNA
165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 5
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170 ccctaaaggg actgggcaga gccttccagg actatggttg gactgaagcc ttcagacgtg 180
171 cctcccacca tggctgtgaa gttcctgggg gcaggcacag cagcctgttt tctgacctc 240
172 gttacctttc cactggacac agccaaggtc cgctgcaga tccaggggga gaaccaggcg 300
173 gtccagacgg ccgggctcgt gcagtaccgt ggcgtgctgg gcaccatcct gaccatggtg 360
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175 agcttgcctt ccattcgcct cggcctctat gactccgtca agcagggtga caccctctct 480
176 ggccgcggga actccagcct cactaccctg attttgccg gctgcaccac aggagccatg 540
177 gcggtgacct gtgcccagcc cacagatgtg gtgaaggctc gatttcaggc cagcatacac 600
178 ctccggccat ccaggagcga cagaaaatac agcgggacta tggacgccta cagaaccatc 660
179 gccaggaggg aaggagtcag gggcctgtgg aaaggaactt tgcccaacat catgaggaat 720
180 gctatcgcta actgtgctga ggtggtgacc tacgacatcc tcaaggagaa gctgctggac 780
181 taccacctgc tcaactgaca ctccctctgc cactttgtct ctgccttttg agccggcttc 840
182 tgtgccacag tgggtggcct cccggtggac gtggtgaaga cccggtatat gaactcacct 900
183 ccaggccagt acttcagccc cctcgactgt atgataaaga tgggtggcca ggaggggccc 960
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185 ggcttctttc ttttcgaatg tggctaccgt gggccaacct gggatgtagc ggtgaagagt 1080
186 acagatgtaa atgccacaaa gaagaagttt aaaaaacat gcaaaaaaaa aa 1132
188 <210> SEQ ID NO: 6
189 <211> LENGTH: 275
190 <212> TYPE: PRT
191 <213> ORGANISM: Homo sapiens
193 <400> SEQUENCE: 6
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196 Phe Leu Gly Ala Gly Thr Ala Ala Cys Phe Ala Asp Leu Val Thr Phe
197 20 25 30
198 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile Gln Gly Glu Asn Gln
199 35 40 45
200 Ala Val Gln Thr Ala Arg Leu Val Gln Tyr Arg Gly Val Leu Gly Thr
201 50 55 60
202 Ile Leu Thr Met Val Arg Thr Glu Gly Pro Cys Ser Pro Tyr Asn Gly
203 65 70 75 80
204 Leu Val Ala Gly Leu Gln Arg Gln Met Ser Phe Ala Ser Ile Arg Ile
205 85 90 95
206 Gly Leu Tyr Asp Ser Val Lys Gln Val Tyr Thr Pro Lys Gly Ala Asp
207 100 105 110
208 Asn Ser Ser Leu Thr Thr Arg Ile Leu Ala Gly Cys Thr Thr Gly Ala
209 115 120 125
210 Met Ala Val Thr Cys Ala Gln Pro Thr Asp Val Val Lys Val Arg Phe
211 130 135 140
212 Gln Ala Ser Ile His Leu Gly Pro Ser Arg Ser Asp Arg Lys Tyr Ser
213 145 150 155 160

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217                               180                               185                               190
218 Asn Cys Ala Glu Val Val Thr Tyr Asp Ile Leu Lys Glu Lys Leu Leu
219                               195                               200                               205
220 Asp Tyr His Leu Leu Thr Asp Asn Phe Pro Cys His Phe Val Ser Ala
221                               210                               215                               220
222 Phe Gly Ala Gly Phe Cys Ala Thr Val Val Ala Ser Pro Val Asp Val
223 225                               230                               235                               240
224 Val Lys Thr Arg Tyr Met Asn Ser Pro Pro Gly Gln Tyr Phe Ser Pro
225                               245                               250                               255
226 Leu Asp Cys Met Ile Lys Met Val Ala Gln Glu Gly Pro Thr Ala Phe
227                               260                               265                               270
228 Tyr Lys Gly
229                               275

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date